IN THE SPECIFICATION:

On p. 2, l. 16, delete "is required".

On p. 6, l. 23, replace the blank with "the Division of Biological Sciences for the University of Missouri".

IN THE CLAIMS:

1. (Amended) A <u>computer-implemented</u> method for identifying relative binding motifs of peptide-like molecules, comprising the steps of:

    (a)   training [an] <u>a computer-implemented</u> artificial neural network (ANN) with <u>input data characterizing</u> a set of training peptide-like molecules, each of known sequence and binding affinity;

    (b)   applying to the ANN <u>input data characterizing</u> at least one <u>test</u> peptide-like molecule, each of known sequence but unknown binding affinity;

    (c)   analyzing each applied test peptide-like molecule using the ANN to [predict] <u>generate a prediction of</u> a relative binding affinity for each test peptide-like molecule, <u>and outputting such prediction</u>.

2. (Amended) A <u>computer-implemented</u> method for identifying relative peptide binding motifs, comprising the steps of:

    (a)   training [an] <u>a computer-implemented</u> artificial neural network (ANN) with <u>input data characterizing</u> a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

    (b)   applying to the ANN <u>input data characterizing</u> at least one <u>test</u> peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

    (c)   analyzing each applied test peptide using the ANN to [predict] <u>generate a prediction of</u> a relative binding affinity for each test peptide, <u>and outputting such prediction</u>.

(Amended) The method of claim 2, wherein the set of training peptides include peptides having a binding affinity for [MHC] major histocompatiblity complex (MHC) class I molecules.

(*Reiterated*) The method of claim 3, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

(*Reiterated*) The method of claim 2, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

(*Reiterated*) The method of claim 5, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

(*Reiterated*) The method of claims 1 or 2, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

8.   A <u>computer-implemented</u> system for identifying relative binding motifs for peptide-like molecules, comprising:

(a)   means for training [an] <u>a computer-implemented</u> artificial neural network (ANN) with <u>input data characterizing</u> a set of training peptide-like molecules, each of known sequence and binding affinity;

(b)   means for applying to the ANN <u>input data characterizing</u> at least one test peptide-like molecule, each of known sequence but unknown binding affinity;

(c)   means for analyzing each applied test peptide-like molecule using the ANN to [predict] <u>generate a prediction of</u> a relative binding affinity for each test peptide-like molecule, <u>and output such prediction</u>.

A <u>computer-implemented</u> system for identifying relative peptide binding motifs, comprising:

(a)   means for training [an] <u>a computer-implemented</u> artificial neural network (ANN) with <u>input data characterizing</u> a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(b)   means for applying to the ANN <u>input data characterizing</u> at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(c)   means for analyzing each applied test peptide using the ANN to [predict] <u>generate a prediction of</u> a relative binding affinity for each test peptide, <u>and output such prediction</u>.

(Amended) The system of claim 9, wherein the set of training peptides include peptides having a binding affinity for [MHC] major histocompatiblity complex (MHC) class I molecules.

(Reiterated) The system of claim 10, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

(Reiterated) The system of claim 9, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

(Reiterated) The system of claim 12, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

(Reiterated) The system of claims 8 or 9, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

15.   (Amended) A computer program, residing on a computer-readable medium, for identifying relative binding motifs for peptide-like molecules, comprising instructions for causing a computer to:

(a)   train [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptide-like molecules, each of known sequence and binding affinity;

(b)   apply to the ANN input data characterizing at least one test peptide-like molecule, each of known sequence but unknown binding affinity;

(c)   analyze each applied test peptide-like molecule using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide-like molecule, and output such prediction.

16.   (Amended) A computer program, residing on a computer-readable medium, for identifying relative peptide binding motifs, comprising instructions for causing a computer to:

(a)   train [an] a computer-implemented artificial neural network (ANN) with input data characterizing a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(b)   apply to the ANN input data characterizing at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;

(c)   analyze each applied test peptide using the ANN to [predict] generate a prediction of a relative binding affinity for each test peptide, and output such prediction.

17. (Amended) The computer program of claim 16, wherein the set of training peptides having a binding affinity for [MHC] <u>major histocompatiblity complex (MHC)</u> class I molecules.

18. (*Reiterated*) The computer program of claim 17, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K^b.

19. (*Reiterated*) The computer program of claim 16, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.

20. (*Reiterated*) The computer program of claim 19, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K^b.

21. (*Reiterated*) The computer program of claims 15 or 16, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.